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<!--StartFragment-->RESULT 1                                APPENDIX A: ALIGNMENT WITH SEQ ID NO 24
ADC00348
ID   ADC00348 standard; protein; 441 AA.                      APPENDIX B: SEQ ID NO, 24
XX
AC   ADC00348;
XX
DT   15-JUN-2007   (revised)
DT   04-DEC-2003   (first entry)
XX
DE   Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 393.
XX
KW   enterohaemorrhagic; anti-bacterial; BOND_PC; hypothetical protein;
KW   hypothetical protein ECs1812 [Escherichia coli O157:H7];
KW   hypothetical protein ECs1812 [Escherichia coli O157:H7 str. Sakai];
KW   unknown protein encoded by cryptic prophage CP-933P;
KW   hypothetical protein [Escherichia coli O157:H7 str. Sakai].
XX
OS   Escherichia coli; O157:H7.
XX
PN   JP2002355074-A.
XX
PD   10-DEC-2002.
XX
PF   24-JAN-2002; 2002JP-00015959.
XX
PR   24-JAN-2001; 2001JP-00112010.
XX
PA   (UYTS-) UNIV TSUKUBA.
XX
DR   WPI; 2003-451640/43.
DR   PC:NCBI; gil3259568.
XX
PT   Enterohemorrhagic Escherichia coli O157:H7-specific nucleic acid molecule
PT   and a polypeptide and its use, a polypeptide, a vector and a host cell.
XX
PS   Claim 3; SEQ ID NO 393; 2067pp; Japanese.
XX
CC   The invention relates to a novel enterohaemorrhagic Escherichia coli
CC   O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
CC   has anti-bacterial activity. The polypeptide can be used in detection
CC   and/or treatment of O157:H7 infection. The nucleotide sequence of the
CC   genome of Enterohaemorrhagic E coli O157:H7 was determined. The present
CC   sequence represents an E. coli O157:H7-specific polypeptide of the
CC   invention.
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 441 AA;
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Query Match          100.0%;   Score 2341;   DB 6;   Length 441;
Best Local Similarity 100.0%;   Pred. No. 1.1e-197;
Matches 441; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
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```
Qy      1 MNIQPTIQSGITSQNNQHHQTEQIPSTQIPQSELPLGCQAGFVFNIPDDIQQHAPECGET 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MNIQPTIQSGITSQNNQHHQTEQIPSTQIPQSELPLGCQAGFVFNIPDDIQQHAPECGET 60

Qy     61 TALLSLIKDKGLLSGLDEYIAPHLEEGSIGKKTLDMFGLFNVTQMALEIPSSVSGISGKY 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TALLSLIKDKGLLSGLDEYIAPHLEEGSIGKKTLDMFGLFNVTQMALEIPSSVSGISGKY 120

Qy    121 GVQLNIVKPDIHPTSGNYFLQIFPLHDEIGFNFKDLPGPLKNALSNSNISTTAVSTIAST 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GVQLNIVKPDIHPTSGNYFLQIFPLHDEIGFNFKDLPGPLKNALSNSNISTTAVSTIAST 180

Qy    181 GTSATTSTVTTEPKDPIPWFLTAQVVRNHGVELPIVKTENGWKLVGETPLTPDGPKANY 240
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      |||
Db      181 GTSATTSTVTTEPKDPIPWFGLTAQVVRNHGVELPIVKTENGWKLVGGETPLTPDGPKANY 240
      |||
Qy      241 TEEWVIRPGEADFKYGASPLQATLGLEFGAHFKWDLNPNNTKYAVLTNAAANALGALGGF 300
      |||
Db      241 TEEWVIRPGEADFKYGASPLQATLGLEFGAHFKWDLNPNNTKYAVLTNAAANALGALGGF 300
      |||
Qy      301 AVSRFASTDPMLSPHIGAMVGQAAGHAIQYNTPLKPDITLWWAGATLGAADLNKAEFEV 360
      |||
Db      301 AVSRFASTDPMLSPHIGAMVGQAAGHAIQYNTPLKPDITLWWAGATLGAADLNKAEFEV 360
      |||
Qy      361 ARFTDYPRIWWHAREGAIFPNKADIEHATGADIRAMEEGIPVGQRHPNPEDVVIDIESNG 420
      |||
Db      361 ARFTDYPRIWWHAREGAIFPNKADIEHATGADIRAMEEGIPVGQRHPNPEDVVIDIESNG 420
      |||
Qy      421 LPHHNPSNHVDIFDIIQETRV 441
      |||
Db      421 LPHHNPSNHVDIFDIIQETRV 441
<!--EndFragment-->
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